

NEW	10	20	30	40	50	60
HNC DNA . SEQ	ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCCGGCC					
HN . SEQ	ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCTGGCTCCCTCTGTTGATCCCCGGCC					
OLD	10	20	30	40	50	80
HNC DNA . SEQ	CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT					
HN . SEQ	CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT					
	70	80	90	100	110	120
HNC DNA . SEQ	CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGAGGAGGCTCTTCTGGGGAA					
HN . SEQ	CCCCAGAGGTTGCCCCGGATGCAGGAGGATTCCCCCTTGGAGGAGGCTCTTCTGGGGAA					
	130	140	150	160	170	180
HNC DNA . SEQ	GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT					
HN . SEQ	GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT					
	180	190	200	210	220	230
HNC DNA . SEQ	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT					
HN . SEQ	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT					
	240	250	260	270	280	290
HNC DNA . SEQ	GAAGTTAAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGT					
HN . SEQ	GAAGTTAATGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGT					
	300	310	320	330	340	350
HNC DNA . SEQ	TGAGGCTCCTGGAGATCCTCAAGAACCCAGATAATGCCACAGGGACAAAGAAGGGGA					
HN . SEQ	TGAGGCTCCTGGAGATCCTCAAGAACCCAGATAATGCCACAGGGACAAAGAAGGGGA					
	360	370	380	390	400	410
HNC DNA . SEQ	TGACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCTGGCCCCGGGTGTCCCCAGCCTG					
HN . SEQ	TGACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCTGGCCCCGGGTGTCCCCAGCCTG					
	420	430	440	450	460	470
HNC DNA . SEQ	CGCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCAGCTCGCCGCCTTCTGCCCCGGC					
HN . SEQ	CGCGGGCCGCTTCCAGTCCCCGGTGGATATCCGCCCCAGCTCGCCGCCTTCTGCCCCGGC					
	480	490	500	510	520	530
HNC DNA . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					
HN . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					
	540	550	560	570	580	590
HNC DNA . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					
HN . SEQ	CCTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCCAGAACTGCGCCTGCG					

	600	610	620	630	640	650
HNCDNA . SEQ	QAA CAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCC					
MN . SEQ	AQA CAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCC					
	600	610	620	630	640	650
HNCDNA . SEQ	CGGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGG					
MN . SEQ	CGGGCGGGAGTACC-GGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTCGTCCGGG					
	660	670	680	690	700	710
HNCDNA . SEQ	CTCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAG					
MN . SEQ	CTCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACCTCAG					
	720	730	740	750	760	770
HNCDNA . SEQ	CACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGGC					
MN . SEQ	CACCGCCTTTGCCAGAGTTGACGAGGCCTTGGGGCGCCCGGGAGGCCTGGCCGTGTTGG-					
	780	790	800	810	820	830
HNCDNA . SEQ	CGCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTG-CCTATGAGCAGTTGCTGTCTCGCT					
MN . SEQ	CGCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGTCCTATGAGCAGTTGCTGTCTCGCT					
	840	850	860	870	880	890
HNCDNA . SEQ	TGAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCAC					
MN . SEQ	TGAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCAC					
	900	910	920	930	940	950
HNCDNA . SEQ	TCCTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCT					
MN . SEQ	TCCTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCT					
	960	970	980	990	1000	1010
HNCDNA . SEQ	GTGCCCAGGGTGTTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGC					
MN . SEQ	GTGCCCAGGGTGTTCATCTGGACTGTGTTTAACCAGACAGTGATGCTGAGTGCTAAGCAGC					
	1020	1030	1040	1050	1060	1070
HNCDNA . SEQ	TCCACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCC					
MN . SEQ	TCCACACCCTCTCTGACACCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCC					
	1080	1090	1100	1110	1120	1130
HNCDNA . SEQ	GAGCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACA					
MN . SEQ	GAGCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACA					
	1140	1150	1160	1170	1180	1190

MNCDNA . SEQ	1200	1210	1220	1230	1240	1250
	GCAGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCC					
MN . SEQ	GCAGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCC					
	1200	1210	1220	1230	1240	1250
MNCDNA . SEQ	1260	1270	1280	1290	1300	1310
	TAGCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGA					
MN . SEQ	TAGCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGA					
	1260	1270	1280	1290	1300	1310
MNCDNA . SEQ	1320	1330	1340	1350	1360	1370
	GAAGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGC-TACCGCCCAGCAGAGGTAGCC					
MN . SEQ	GAAGGCAGCACAGAAGGGGAACCAAAGGGGGTGTGAGCGTACCGCCCAGCAGAGGTAGCC					
	1320	1330	1340	1350	1360	1370
MNCDNA . SEQ	1380	1390	1400	1410	1420	1430
	GAGACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGA					
MN . SEQ	GAGACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGA					
	1380	1390	1400	1410	1420	1430
MNCDNA . SEQ	1440	1450	1460	1470	1480	1490
	GGGGGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAA					
MN . SEQ	GGGGGAGCCGGTAACTGTCCTGTCCTGCTCATTATGCCACTTCCTTTTAACTGCCAAGAA					
	1440	1450	1460	1470	1480	1490
MNCDNA . SEQ	1500	1510	1520			
	ATTTTTTAAAATAAATATTTATAAT					
MN . SEQ	ATTTTTTAAAATAAATATTTATAAT					
	1500	1510	1520			